

SEQUENCE LISTING

<110> Tsuji, Takashi
Tezuka, Katsunari
Hori, Nobuaki

<120> HUMAN MONOCLONAL ANTIBODY AGAINST A
COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
PHARMACEUTICAL USE THEREOF

<130> 06501-079001

<140> US 09/859,053

<141> 2001-05-16

<150> JP 2001-99508

<151> 2001-03-30

<150> JP 2000-147116

<151> 2000-05-18

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	Met	Asp	Trp	Thr	Trp	Arg Ile Leu Phe Leu Val Ala Ala Ala	
			-15			-10	
aca gga gcc	cac tcc	cag gtg	cag ctg	gtg cag	tct ggg	gct gag gtg	158
Thr Gly Ala	His Ser	Gln Val	Gln Leu	Val Gln	Ser Gly	Ala Glu Val	
-5		1		5		10	
aag aag cct	ggg gcc	tca gtg	aag gtc	tcc tgc	aag gct	tct gga tac	206
Lys Lys Pro	Gly Ala	Ser Val	Lys Val	Ser Cys	Lys Ala	Ser Gly Tyr	
	15		20		25		
acc ttc acc	ggc tac	tat atg	cac tgg	gtg cga	cag gcc	cct gga caa	254
Thr Phe Thr	Gly Tyr	Tyr Met	His Trp	Val Arg	Gln Ala	Pro Gly Gln	
	30		35		40		
ggg ctt gag	tgg atg	gga tgg	atc aac	cct cac	agt ggt	ggc aca aac	302
Gly Leu Glu	Trp Met	Gly Trp	Ile Asn	Pro His	Ser Gly	Gly Thr Asn	
	45		50		55		
tat gca cag	aag ttt	cag ggc	agg gtc	acc atg	acc agg	gac acg tcc	350
Tyr Ala Gln	Lys Phe	Gln Gly	Arg Val	Thr Met	Thr Arg	Asp Thr Ser	
	60		65		70		75
atc agc aca	gcc tac	atg gag	ctg agc	agg ctg	aga tcc	gac gac acg	398
Ile Ser Thr	Ala Tyr	Met Glu	Leu Ser	Arg Leu	Arg Ser	Asp Asp Thr	
	80		85		90		
gcc gtg tat	tac tgt	gcg agg	acg tat	tac tat	gat agt	agt ggt tat	446
Ala Val Tyr	Tyr Cys	Ala Arg	Thr Tyr	Tyr Tyr	Asp Ser	Ser Gly Tyr	
	95		100		105		
tac cat gat	gct ttt	gat atc	tgg ggc	caa ggg	aca atg	gtc acc gtc	494
Tyr His Asp	Ala Phe	Asp Ile	Trp Gly	Gln Gly	Thr Met	Val Thr Val	
	110		115		120		
tct tca gcc	tcc acc	aag ggc	cca tcg	gtc ttc	ccc ctg	gcg ccc tgc	542
Ser Ser Ala	Ser Thr	Lys Gly	Pro Ser	Val Phe	Pro Leu	Ala Pro Cys	
	125		130		135		
tcc agg agc	acc tcc	gag agc	aca gcg	gcc ctg	ggc tgc	ctg gtc aag	590
Ser Arg Ser	Thr Ser	Glu Ser	Thr Ala	Ala Leu	Gly Cys	Leu Val Lys	
	140		145		150		155
gac tac ttc	ccc gaa	ccg gtg	acg gtg	tcg tgg	aac tca	ggc gct ctg	638
Asp Tyr Phe	Pro Glu	Pro Val	Thr Val	Ser Trp	Asn Ser	Gly Ala Leu	
	160		165		170		
acc agc ggc	gtg cac	acc ttc	cca gct	gtc cta	cag tcc	tca gga ctc	686
Thr Ser Gly	Val His	Thr Phe	Pro Ala	Val Leu	Gln Ser	Ser Gly Leu	
	175		180		185		

tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc aac ttc ggc acc	734
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr	
190 195 200	
cag acc tac acc tgc aac gta gat cac aag ccc agc aac acc aag gtg	782
Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val	
205 210 215	
gac aag aca gtt gag cgc aaa tgt tgt gtc gag tgc cca ccg tgc cca	830
Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro	
220 225 230 235	
gca cca cct gtg gca gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc	878
Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro	
240 245 250	
aag gac acc ctc atg atc tcc cgg acc cct gag gtc acg tgc gtg gtg	926
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val	
255 260 265	
gtg gac gtg agc cac gaa gac ccc gag gtc cag ttc aac tgg tac gtg	974
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val	
270 275 280	
gac ggc gtg gag gtg cat aat gcc aag aca aag cca cgg gag gag cag	1022
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln	
285 290 295	
ttc aac agc acg ttc cgt gtg gtc agc gtc ctc acc gtt gtg cac cag	1070
Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln	
300 305 310 315	
gac tgg ctg aac ggc aag gag tac aag tgc aag gtc tcc aac aaa ggc	1118
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly	
320 325 330	
ctc cca gcc ccc atc gag aaa acc atc tcc aaa acc aaa ggg cag ccc	1166
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro	
335 340 345	
cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc	1214
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr	
350 355 360	
aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc	1262
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser	
365 370 375	
gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac	1310
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr	
380 385 390 395	
aag acc aca cct ccc atg ctg gac tcc gac ggc tcc ttc ttc ctc tac	1358
Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr	
400 405 410	
agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc	1406

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 415 420 425

tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag 1454
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 430 435 440

agc ctc tcc ctg tct ccg ggt aaa tgagtgccac ggccggcaag cccccgctcc 1508
 Ser Leu Ser Leu Ser Pro Gly Lys
 445 450

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<400> 28

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 35 40 45
 Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60
 Glu Trp Met Gly Trp Ile Asn Pro His Ser Gly Gly Thr Asn Tyr Ala
 65 70 75 80
 Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser
 85 90 95
 Thr Ala Tyr Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Thr Tyr Tyr Tyr Asp Ser Ser Gly Tyr Tyr His
 115 120 125
 Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 130 135 140
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 145 150 155 160
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 165 170 175
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 180 185 190
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 195 200 205
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
 210 215 220
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 225 230 235 240
 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
 245 250 255
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 260 265 270
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 275 280 285
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly

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Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn				
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Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp				
	325		330	335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro				
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Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu				
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Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn				
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Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile				
385		390		395
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr				
	405		410	415
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys				
	420		425	430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys				
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Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu				
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 Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Phe Pro Gly Ser Arg Cys
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gac atc cag atg acc cag tct cca tct tcc gtg tct gca tct gta gga 152
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
 1 5 10 15

gac aga gtc acc atc act tgt cgg gcg agt cag ggt att agc agg ttg 200
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Arg Leu

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tat gtt gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agc ggc Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly 50 55 60			296
agt gga tct ggg aca gat ttc act ctc acc atc agc agc ctg cag cct Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro 65 70 75 80			344
gaa gat ttt gca act tac tat tgt caa cag gct aac agt ttc ccg tgg Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Trp 85 90 95			392
acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala 100 105 110			440
cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly 115 120 125			488
act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala 130 135 140			536
aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln 145 150 155 160			584
gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser 165 170 175			632
agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr 180 185 190			680
gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser 195 200 205			728
ttc aac agg gga gag tgt tagagggaga agtgccccca cctgctcctc Phe Asn Arg Gly Glu Cys 210			776
agttccagcc tgacccccctc ccatacctttg gcctctgacc ctttttccac aggggaccta cccctattgc ggtcctccag ctcatactttc acctaccccc cctcctcctc cttggcttta attatgctaa tgttggagga gaatgaataa ataaagtga tctttgcaaa aaaaaaaaaa aaaaatctct gcggccgc			836 896 956 974

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<212> PRT

<213> Homo sapiens

<400> 30

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Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
          35           40           45
Gln Gly Ile Ser Arg Leu Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
          50           55           60
Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
65           70           75           80
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
          85           90           95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
          100          105          110
Ala Asn Ser Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
          115          120          125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
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Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145          150          155          160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
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Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
          180          185          190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
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<222> (1507)...(1708)

<221> sig_peptide

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<221> misc_feature

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<223> n = A,T,C or G

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Met Glu Leu Gly Leu Ser Trp	
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gtt ttc ctt gtt gct ata tta gaa ggt gtc cag tgt gag gtg cag ctg	162
Val Phe Leu Val Ala Ile Leu Glu Gly Val Gln Cys Glu Val Gln Leu	
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gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc ctg aga ctc	210
Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu	
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tcc tgt gca gcc tct gga ttc acc ttc agt agc tac gac atg cac tgg	258
Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met His Trp	
25 30 35	
gtc cgc caa gct aca gga aaa ggt ctg gag tgg gtc tca gct att ggt	306
Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Gly	
40 45 50	
act gct ggt gac aca tac tat cca ggc tcc gtg aag ggc cga ttc acc	354
Thr Ala Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys Gly Arg Phe Thr	
55 60 65	
atc tcc aga gaa aat gcc aag aac tcc ttg tat ctt caa atg aac agc	402
Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser	
70 75 80	
ctg aga gcc ggg gac acg gct gtg tat tac tgt gta aga gat aat agg	450
Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Val Arg Asp Asn Arg	
85 90 95 100	
aag gtg acc cac gag cac tac tac tac tac ggt atg gac gtc tgg ggc	498
Lys Val Thr His Glu His Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly	
105 110 115	
caa ggg acc acg gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg	546
Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	
120 125 130	
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Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala	
135 140 145	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg	642
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	
150 155 160	
tcg tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca gct	690
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	
165 170 175 180	
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg	738
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val	
185 190 195	

ccc tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat cac Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His 200 205 210	786
aag ccc agc aac acc aag gtg gac aag aca gtt gag cgc aaa tgt tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys 215 220 225	834
gtc gag tgc cca ccg tgc cca gca cca cct gtg gca gga ccg tca gtc Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val 230 235 240	882
ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr 245 250 255 260	930
cct gag gtc acg tgc gtg gtg gtg gac gtg agc cac gaa gac ccc gag Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu 265 270 275	978
gtc cag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys 280 285 290	1026
aca aag cca cgg gag gag cag ttc aac agc acg ttc cgt gtg gtc agc Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser 295 300 305	1074
gtc ctc acc gtt gtg cac cag gac tgg ctg aac ggc aag gag tac aag Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys 310 315 320	1122
tgc aag gtc tcc aac aaa ggc ctc cca gcc ccc atc gag aaa acc atc Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile 325 330 335 340	1170
tcc aaa acc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro 345 350 355	1218
cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu 360 365 370	1266
gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag tgg gag agc aat Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn 375 380 385	1314
ggg cag ccg gag aac aac tac aag acc aca cct ccc atg ctg gac tcc Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser 390 395 400	1362
gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg 405 410 415 420	1410

tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg 1458
 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 425 430 435

cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa 1503
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 440 445 450

tgagtgccac ggccggcaag cccccgtccc ccaggctctc ggggtcgcgt gaggatgctt 1563
 ggcacgtacc ccgtgtacat acttcccagg caccagcat ggaaataaag caccagcgc 1623
 tgccctgggc ccctgcnaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1683
 aaaaaaaaaa aatctctgcg gccgc 1708

<210> 32
 <211> 470
 <212> PRT
 <213> Homo sapiens

<400> 32
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 1 5 10 15
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45
 Ser Ser Tyr Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu
 50 55 60
 Glu Trp Val Ser Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly
 65 70 75 80
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser
 85 90 95
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr
 100 105 110
 Tyr Cys Val Arg Asp Asn Arg Lys Val Thr His Glu His Tyr Tyr Tyr
 115 120 125
 Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 130 135 140
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 145 150 155 160
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 165 170 175
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 180 185 190
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 195 200 205
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
 210 215 220
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 225 230 235 240
 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
 245 250 255
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 260 265 270
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 275 280 285
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 290 295 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
 305 310 315 320
 Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
 325 330 335
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
 340 345 350
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
 355 360 365
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
 370 375 380
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 385 390 395 400
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 405 410 415
 Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 420 425 430
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 435 440 445
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 450 455 460
 Ser Leu Ser Pro Gly Lys
 465 470

<210> 33
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
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<221> CDS
 <222> (28)...(735)

<221> 3'UTR
 <222> (739)...(948)

<221> sig_peptide
 <222> (28)...(87)

<221> misc_feature
 <222> (1)...(948)
 <223> n = A,T,C or G

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 gaattcgag tgccatgaca ccacgcc atg gaa acc cca gcg cag ctt ctc ttc 54
 Met Glu Thr Pro Ala Gln Leu Leu Phe
 -20 -15

ctc ctg cta ctc tgg ctc cca gat acc acc gga gaa att gtg ttg acg 102
 Leu Leu Leu Leu Trp Leu Pro Asp Thr Thr Gly Glu Ile Val Leu Thr
 -10 -5 1 5

cag tct cca ggc acc ctg tct ttg tct cca ggg gaa aga gcc acc ctc 150
 Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu
 10 15 20

tcc tgc agg gcc agt cag aat att aga agc agc tac tta gcc tgg tac Ser. Cys Arg Ala Ser Gln Asn Ile Arg Ser Ser Tyr Leu Ala Trp Tyr 25 30 35	198
cag cag aaa cct ggc cag gct ccc ggg ctc ctc atc tat ggt gca tcc Gln Gln Lys Pro Gly Gln Ala Pro Gly Leu Leu Ile Tyr Gly Ala Ser 40 45 50	246
agc agg gcc act ggc atc cca gac agg ttc agt ggc agt ggg tct ggg Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly 55 60 65	294
aca gac ttc act ctc acc atc agc aga ctg gag cct gaa gat ttt gca Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala 70 75 80 85	342
gtg tat tac tgt cag cag ttt ggt agc tca cct atg tgc agt ttt ggc Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro Met Cys Ser Phe Gly 90 95 100	390
cag ggg acc aag ctg gag atc aaa cga act gtg gct gca cca tct gtc Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val 105 110 115	438
ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser 120 125 130	486
gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln 135 140 145	534
tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val 150 155 160 165	582
aca gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu 170 175 180	630
acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu 185 190 195	678
gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg 200 205 210	726
gga gag tgt tagagggaga antgccccca cctgctctc agttccagcc Gly Glu Cys 215	775
tgacccccctc ccatacctttg gcctctgacc ctttttccac aggggaccta cccctattgc ggctctccag ctcatctttc acctcaccac cctcctctc cttggcttta attatgctaa tgttgaggga gaatgaataa ataaagtga tctttgcacc tgtgaaaaaa aaa	835 895 948

<210> 34
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 34
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 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
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 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Asn
 35 40 45
 Ile Arg Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 50 55 60
 Pro Gly Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro
 65 70 75 80
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 85 90 95
 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe
 100 105 110
 Gly Ser Ser Pro Met Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
 115 120 125
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 130 135 140
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 145 150 155 160
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 165 170 175
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 180 185 190
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 195 200 205
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 210 215 220
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 35
 <211> 1673
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(95)

 <221> CDS
 <222> (96)...(1505)

 <221> 3'UTR
 <222> (1509)...(1673)

 <221> sig_peptide
 <222> (96)...(152)

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attcagtgat caggactgaa cacacaggac tcacc atg gag ttg ggg ctg agc	113
Met Glu Leu Gly Leu Ser	
-15	
tggtgtttttctt gtt gct ata tta gaa ggt gtc cag tgt gag gtg cag	161
Trp Val Phe Leu Val Ala Ile Leu Glu Gly Val Gln Cys Glu Val Gln	
-10 -5 1	
ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc ctg aga	209
Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg	
5 10 15	
ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tac gac atg cac	257
Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Asp Met His	
20 25 30 35	
tggtgtc cgc caa gct aca gga aaa ggt ctg gag tgg gtc tca gct att	305
Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Val Ser Ala Ile	
40 45 50	
ggt act gct ggt gac aca tac tat cca ggc tcc gtg aag ggc cga ttc	353
Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly Ser Val Lys Gly Arg Phe	
55 60 65	
acc atc tcc aga gaa aat gcc aag aac tcc ttg tat ctt caa atg aac	401
Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn	
70 75 80	
agc ctg aga gcc ggg gac acg gct gtg tat tac tgt gta aga gat aag	449
Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys Val Arg Asp Lys	
85 90 95	
agg acg gtg acc cac gag cac tac tac tac tac ggt atg gac gtc tgg	497
Arg Thr Val Thr His Glu His Tyr Tyr Tyr Tyr Gly Met Asp Val Trp	
100 105 110 115	
ggc caa ggg acc acg gtc acc gtc tcc tca gcc tcc acc aag ggc cca	545
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro	
120 125 130	
tcg gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag agc aca	593
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr	
135 140 145	
gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acc	641
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr	
150 155 160	
gtg tcg tgg aac tca ggc gct ctg acc agc ggc gtg cac acc ttc cca	689
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro	
165 170 175	
gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc	737
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr	
180 185 190 195	
gtg ccc tcc agc aac ttc ggc acc cag acc tac acc tgc aac gta gat	785

Val	Pro	Ser	Ser	Asn	Phe	Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn	Val	Asp		
				200					205					210			
cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aca	gtt	gag	cgc	aaa	tgt	833	
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Glu	Arg	Lys	Cys		
			215					220					225				
tgt	gtc	gag	tgc	cca	ccg	tgc	cca	gca	cca	cct	gtg	gca	gga	ccg	tca	881	
Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	Gly	Pro	Ser		
			230					235					240				
gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	929	
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg		
			245				250					255					
acc	cct	gag	gtc	acg	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	ccc	977	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro		
			260			265				270					275		
gag	gtc	cag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	1025	
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala		
				280					285						290		
aag	aca	aag	cca	cgg	gag	gag	cag	ttc	aac	agc	acg	ttc	cgt	gtg	gtc	1073	
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Val	Val		
			295					300					305				
agc	gtc	ctc	acc	gtt	gtg	cac	cag	gac	tgg	ctg	aac	ggc	aag	gag	tac	1121	
Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr		
			310					315					320				
aag	tgc	aag	gtc	tcc	aac	aaa	ggc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	1169	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr		
			325				330					335					
atc	tcc	aaa	acc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	1217	
Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu		
					345					350					355		
ccc	cca	tcc	cgg	gag	gag	atg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	1265	
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys		
					360					365					370		
ctg	gtc	aaa	ggc	ttc	tac	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	1313	
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser		
				375				380					385				
aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	aca	cct	ccc	atg	ctg	gac	1361	
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Met	Leu	Asp		
			390					395					400				
tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	1409	
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser		
			405				410					415					
agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	1457	
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala		

420 425 430 435 1505
 ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 440 445 450

tgagtgccac ggccggcaag cccccgctcc ccaggctctc ggggtcgcgt gaggatgctt 1565
 ggacgtacc ccgtgtacat acttcccagg caccagcat ggaaataaag caccagcgc 1625
 tgccctgggc ccctgcgaaa aaaaaaaaaa aaaaatctct gcggccgc 1673

<210> 36
 <211> 470
 <212> PRT
 <213> Homo sapiens

<400> 36
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 1 5 10 15
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45
 Ser Ser Tyr Asp Met His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu
 50 55 60
 Glu Trp Val Ser Ala Ile Gly Thr Ala Gly Asp Thr Tyr Tyr Pro Gly
 65 70 75 80
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn Ser
 85 90 95
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr
 100 105 110
 Tyr Cys Val Arg Asp Lys Arg Thr Val Thr His Glu His Tyr Tyr Tyr
 115 120 125
 Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 130 135 140
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 145 150 155 160
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 165 170 175
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 180 185 190
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 195 200 205
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
 210 215 220
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 225 230 235 240
 Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
 245 250 255
 Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 260 265 270
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 275 280 285
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 290 295 300
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
 305 310 315 320
 Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp

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          325          330          335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
          340          345          350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
          355          360          365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
          370          375          380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
          385          390          395          400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
          405          410          415
Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
          420          425          430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
          435          440          445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
          450          455          460
Ser Leu Ser Pro Gly Lys
          465          470

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<210> 37
<211> 970
<212> DNA
<213> Homo sapiens

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<220>
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<222> (1)...(32)

<221> CDS
<222> (33)...(740)

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<221> 3'UTR
<222> (744)...(970)

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<221> sig_peptide
<222> (33)...(92)

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<400> 37
gaattcgag tgccatgaca ccacggggaa cc atg gaa acc cca ggc cag ctt      53
                               Met Glu Thr Pro Ala Gln Leu
                               -20                               -15

ctc ttc ctc ctg cta ctc tgg ctc cca gat acc acc gga gaa att gtg      101
Leu Phe Leu Leu Leu Leu Trp Leu Pro Asp Thr Thr Gly Glu Ile Val
          -10          -5          1

ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg gaa aga gcc      149
Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala
          5          10          15

acc ctc tcc tgc agg gcc agt cag agt att agc agc agc tcc tta gcc      197
Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Ser Ser Ser Leu Ala
          20          25          30          35

tgg tac cag cag aaa cct ggc cag gct ccc ggg ctc ctc atc ttt ggt      245
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Gly Leu Leu Ile Phe Gly

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40	45	50	
gca tcc agc agg gcc act ggc atc cca gac agg ttc agt ggc agt ggg			293
Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly			
55	60	65	
tct ggg aca gac ttc act ctc acc atc agc aga ctg gag cct gaa gat			341
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp			
70	75	80	
ttt gca gtg tat tac tgt cag cag ttt ggt agc tca cct atg tgc agt			389
Phe Ala Val Tyr Tyr Cys Gln Gln Phe Gly Ser Ser Pro Met Cys Ser			
85	90	95	
ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg gct gca cca			437
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro			
100	105	110	115
tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act			485
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr			
120	125	130	
gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa			533
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys			
135	140	145	
gta cag tgg aag gtg gat aac gcc ctc caa tgg ggt aac tcc cag gag			581
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu			
150	155	160	
agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc agc agc			629
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser			
165	170	175	
acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc			677
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala			
180	185	190	195
tgc gaa gtc acc cat cag ggc ctg agc tgg ccc gtc aca aag agc ttc			725
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe			
200	205	210	
aac agg gga gag tgt tagagggaga agtgccccc cctgctctc agttccagcc			780
Asn Arg Gly Glu Cys			
215			
tgacccccctc ccatacctttg gcctctgacc ctttttccac aggggaccta cccctattgc			840
ggtcctccag ctcatactttc acctcaccac cctcctctctc cttggcttta attatgctaa			900
tgattggagga gaatgaataa ataaagtga tcttttgcaaa aaaaaaaaaa aaaaaaatct			960
ctgcggccgc			970

<210> 38

<211> 236

<212> PRT

<213> Homo sapiens

<400> 38

Met	Glu	Thr	Pro	Ala	Gln	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Trp	Leu	Pro
1				5				10						15	
Asp	Thr	Thr	Gly	Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser
			20					25					30		
Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser
		35					40					45			
Ile	Ser	Ser	Ser	Ser	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala
	50					55					60				
Pro	Gly	Leu	Leu	Ile	Phe	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro
65					70					75				80	
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile
				85					90					95	
Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Phe
			100					105					110		
Gly	Ser	Ser	Pro	Met	Cys	Ser	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile
		115					120					125			
Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp
	130					135					140				
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn
145					150					155				160	
Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu
			165						170					175	
Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp
			180					185					190		
Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr
		195					200					205			
Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser
	210					215					220				
Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
225					230					235					

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<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially synthesized primer sequence

<221> primer_bind

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35

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<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificially synthesized primer sequence

<221> primer_bind

<222> (1)...(33)

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33

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Met Tyr Pro Pro Pro Tyr
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<212> PRT
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<400> 42
Tyr Met Asn Met
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<210> 43
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<213> Homo sapiens

<400> 43
Tyr Val Lys Met
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